

SEQUENCE LISTING

<110> MASUDA, ESTEBAN

<120> METHODS OF SCREENING CYCLIC PEPTIDES AND
IDENTIFYING TARGETS THEREFOR

<130> RIGL-023

<140> 10/533,144

<141> 2005-04-27

<150> US03/27370

<151> 2003-08-30

<150> 60/407,385

<151> 2002-08-30

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1227

<212> DNA

<213> Artificial Sequence

<220>

<223> recombinant polynucleotide

<220>

<221> CDS

<222> (1)...(1227)

<220>

<221> misc_feature

<222> 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171

<223> n = A,T,C or G

<400> 1

atg	gag	agc	ggc	agc	ccc	gag	atc	gag	aag	ctg	agt	cag	agc	gac	atc	48
Met	Glu	Ser	Gly	Ser	Pro	Glu	Ile	Glu	Lys	Leu	Ser	Gln	Ser	Asp	Ile	
1				5					10					15		

tac	tgg	gac	agc	atg	gtg	agc	atc	acc	gag	acc	ggc	gtg	gag	gag	gtg	96
Tyr	Trp	Asp	Ser	Met	Val	Ser	Ile	Thr	Glu	Thr	Gly	Val	Glu	Glu	Val	
			20					25					30			

ttc	gac	ctg	acc	gtg	ccc	ggc	ccc	cac	aac	ttc	gtg	gcc	aac	gac	atc	144
Phe	Asp	Leu	Thr	Val	Pro	Gly	Pro	His	Asn	Phe	Val	Ala	Asn	Asp	Ile	
		35					40					45				

atc	gtc	cac	aac	agc	nnn	nnn	nnn	nnn	tgc	atc	agc	ggc	gac	agc	ctg	192
Ile	Val	His	Asn	Ser	Xaa	Xaa	Xaa	Xaa	Cys	Ile	Ser	Gly	Asp	Ser	Leu	
	50					55					60					

atc agc ctg gcc agc acc ggc aag agg gtg agc atc aag gac ctg ctg	240
Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu	
65 70 75 80	
gac gag aag gac ttc gag atc tgg gcc atc aac gag cag acc atg aag	288
Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys	
85 90 95	
cta gag agc gcc aag gtg agc agg gtg ttc tgc acc ggc aag aag cta	336
Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu	
100 105 110	
gtg tac atc cta aga acc agg cta ggc agg acc atc aag gcc acc gcc	384
Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala	
115 120 125	
aac cac agg ttc cta acc atc gac ggc tgg aag agg cta gac gag cta	432
Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu	
130 135 140	
agc cta aag gag cac atc gcc cta ccc cgg aag cta gag agc agc agc	480
Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser	
145 150 155 160	
cta cag cta ggc ctc cgc ggc cag atc gat gtg agc aag ggc gag gag	528
Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu	
165 170 175	
ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta	576
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val	
180 185 190	
aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc	624
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr	
195 200 205	
tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	672
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
210 215 220	
gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg cag tgc	720
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys	
225 230 235 240	
ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc	768
Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser	
245 250 255	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	816
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
260 265 270	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	864
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
275 280 285	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	912
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
290 295 300	

aac atc ctg ggg cac aag ctt gag tac aac ttc aac agc cac aac gtg	960
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
305 310 315 320	
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	1008
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
325 330 335	
atc cgc cac aac atc gag gac gga tcc gtg cag ctc gcc gac cac tac	1056
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
340 345 350	
cag cag aac acc cca att ggc gac ggg ccc gtg ctg ctg ccc gac aac	1104
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
355 360 365	
cac tac ctg agc acc cag agc gct ctt tcg aaa gac ccc aac gag aag	1152
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
370 375 380	
cgc gat cat atg gtc ctg ctc gag ttc gtg acc gcc gcc ggg atc act	1200
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
385 390 395 400	
ctc ggc atg gac gag ctg tac aag taa	1227
Leu Gly Met Asp Glu Leu Tyr Lys *	
405	

<210> 2

<211> 408

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> 54, 55, 56, 57

<223> Xaa = Any Amino Acid

<220>

<223> recombinant polypeptide

<400> 2

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile	
1 5 10 15	
Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val	
20 25 30	
Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile	
35 40 45	
Ile Val His Asn Ser Xaa Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu	
50 55 60	
Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu	
65 70 75 80	
Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys	
85 90 95	
Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu	
100 105 110	
Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala	

